

FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG
CTCTGTTGAGAATC**ATG**CTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC
CTCCCTTTTTGCCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC
AGACTGCAGTAAGTGTTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG
AACTAAG**TAA**ATATATGACTAGAAATAGCTCCACTTTGGGGGAAGACTTGTAGCTGAGCTGAT
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATATACTCAGCATCTTTATCAC
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG
AACCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG
TGTTCAAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAACTCTGAATTC
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTG
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT
ATGGAAATAAACACACCTTTGTAAAGATAAAAAAAA

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP
GIPGNHGNNGNNGATGHEGAKGEKGDKGD LGPRGERGQHGPKEKGYPGIPPELQIAFMASL
ATHFSNQNSGIIFFSSVETNIGNFFDVM TGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG
NTVFSMYSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRSTFAGFLLFETK

Important features of the protein:

Signal peptide:

amino acids 1-22

Motif name: Clq domain signature.

amino acids 137-167

Clq domain proteins.

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG
CTCTGGCAGGCTCCTGGCAGCATGGCGAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT
GGCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTCTTCTGCTGGATGGTTTTTC
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACC
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT
GGCCGGGCGGACCTGGCAGCCATATAACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA
CCAAGTGGATCCAGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCAC
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC
ACTCTGAGATATATAACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTTGGATGAACAGCACCGGCA
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGT
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCT
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC
CACTGTGCCCTGGCACTGATTCTTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTC
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT
TCTATACATAAAAGTTCCTACTTGTTAA

FIGURE 4

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDY
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMLWWNGSEPLW
VTLTAKARKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA
IYHERIDVEGHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFW
MDKVIELNKYISLNDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYY
KKGKFSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI
LLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 5

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC**ATG**ACGCTCCTCC
CCGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGG
GGGCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCA
GGCCCCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGG
TGTCACAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAG
TGCCCGGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACC
CTGGAGATAACGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGT
GCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTG
CGGCTGCTCCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCT
CCCCACACCTGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGCTGCACCT
GCGTGCTGCCCCGTTTCAAGT**TGA**ACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGC
TCCCCAGAGGGCACCCCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACT
ACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGACAGCCCCCCTGTTCTCCTCATCTC
CAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAA
AAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTA
TCACTGGCCTCAGGCCCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCT
TAAACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

FIGURE 6

MTLLPGLLEFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQAL
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKL
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVP
VGCTCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 7

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAACATGCAGCTCGGCACTGGGCTCCTG
CTGGCCGCCGTCCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTACCAAGTGCAC
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCA
CTGCCACCCGGGTCCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATA
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCCTACGTATCCATCGCTTGCTGCCAGAC
CAGCCTCTGCAACCATGACTGACGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCAC
AGCCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCCTCGAGACTGGCCAGCCCACC
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCTAGGGAAGTCCTGCGTGGAGTC
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCTTCAGGTCCC
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623

><subunit 1 of 1, 97 aa, 1 stop

><MW: 10160, pI: 6.56, NX(S/T): 0

MQLG TGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLP

LVTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 9

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAG
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCT
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAG
CTGGGCTCGGGCGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC
TTCTGCCGCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA
CAAAATGGCCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCCTGCCCAGATCTCTACCAGTGGTCTG
ATGGAAGCAATTCCCAGTACCGAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA
ATCCAACAGCCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAAGTA
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA
GAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAATTCTGGATC
TGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAA
GATGAACTGTAAGCTCCCCCTTGAGGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTT
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC
CCAACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTACCTTTTATAAGTTGTTATCTA
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAA
GTGTTTGATAAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTTCAATACAT
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG
TACCATAGAAAAAGTTTGTCTTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCTCCTC
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA
TTATTTTTAGCTTAAAATTAAACAGATTTTGTAAATAATGTAACCTTTGTTAATAGGTGCATAA
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC
TTGCCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC
ATTTTAGGAAGGAAGGAAGTACGAAATCGTGTGAAAATGGGTTGGAACCCATCAGTGATCG
CATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC
TAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCTCTGGTCTTCA
TATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTGTTTCTGGGGGAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFRRVSGQKVCFADFKHPCYKMAYFHELSSRVSFQEARLACE
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDG
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINP
TAPVEKPYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG
RTKTSPNQSTLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

FIGURE 11

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCCTGGTCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTGCTGTGCGAGGCCGGCAGGTGG
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCTGACC
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT
GCCTGGTCCTCAACGTCTATAGCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCTGTG
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC
ACAGAGCCATCACACAGAGTGGGGTCTACACCACCCAGGGATCATCGACTCTCACCCTTGGCCCCCTAGCTCAGA
AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG
AAGAGCTGGTCTTAGCAAGAAGCTGAAAATACTATCTATCCTCTCACCCTTGATGGCACTGTCTTCCCCAAAA
GCCCCAAGGAACTCCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA
GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT
CAACACCCGTCTTGACCAGTCTGGATGTGCCCCCTGAGATGATGCCACCCGTATAGATGAATACCTAGGAAGCA
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCCACCGTCA
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCCAGCATCGACCCAGTTCTTTTG
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGGTCTTTGTGTTCCGAGGTCCCTTCCTCA
TGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG
AACATATCTGGAGATCAACCCAGTGGCACGGGCCGGACAGAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG
AGACGCTCCCCAGCAAGATACAACAGTGGCACAGAGAAGCAGGAAGGCCAGGAGGACCTCTGAGGCC
AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC
CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA
ATGTCACAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT
CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCTTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC
TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
CCCCCTCAGAGGAGCTCTCTCAAAATGGGGATTAGCCTAACCCCACTCTGTCAACCCACACCAGGATCGGGTGGGA
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACTTGAAC
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCACCGACATTGTCCACCCTGGCCAGAAGGGTGCATGCC
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCCCTGGCCCCCTGCACAAGACAACAGA
ATCCATCAGGGCCATGAGTGTACCCAGACCTGACCCTCACCAATTCCAGCCCCCTGACCCTCAGGACGCTGGATG
CCAGCTCCCAGCCCCAGTGCCGGGTCTCCTCCTCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGCATCCGTGCGGCTATTGTACA
GAGAAAAGAAGAGACCCACCCACTCGGGCTGAAAAGGTGAAAAGCACCAAGAGGTTTTTCAGATGGAAGTGAGAG
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGTCTCCTGCGCCTCTGCCTGGGCTCCCACTTTGGCA
GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAGGCCGGAGCCAGCT
CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG
AGTGAGTTCCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGCAGGGCTCGG
GACCTGCAGCCCTCCATGCCTGACCCTCCCCCACCCTCGTGGGCTCCTGTGCGGCGGAGCCTCCCCAAGGAG
CGCCGCCCCCTGCTCCACAGCGCCCAGTCCCATCGACCACCCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG
GGACTTGAGAAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT
TGTAACACACCAATCAGCACCCCTGTGTCTAGCTCAGTGTGTTGTGAATGCACCAATCCACACTCTGTATCTGGCT
ACTCTGGTGGGACTTGAGAAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCCTGTCAAACAGACCACTTGACTCTCTGTAAAT
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC
CCCTCGGGTCCCTCCCACGCCGTGGAAGCTTTGTTCTTTGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLG
IPFAQPPLGPDREFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC
LVLNVYSPA EVPAGSGRPVMVWVHGGALITGAATSYDGSALAAAYGDVVVVTVQYRLGVLGFF
STGDEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFEGGSAGGSIIISGLVLSPPVAAAGLF
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT
IYPLTVDGTVPFKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLD TMEQMSREDMLA
ISTPVLTS LDVPPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW
HQQQKNRKAQEDL

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

FIGURE 13

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAG
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACTAAAATTCCTCAA
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCT
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCCTTCAGCGTG
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATC
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT
CTGAAGGAGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT
TTTTGGAAGTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG
AGGATCTA**TGA**GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG
GTCTCATTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG
CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA
ATGAAGGATTTTTTTTTTAAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAG
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAAGTACT
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG
GAATAAAACACAAATGTTGAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATAT
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTTTAAGTACAGGTTCTTAGTGTTTT
ACTATAACTGTCACCTATGTATGTAAGTACATATATAAATAGTCATTTATAAATGACCGTAT
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAAA

FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLELLQLKFLKPKINSFYAFEVKDAKGRTVSL
EKYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGESEPRPSKEVES
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVVKFWRPEEP
IEVIRPDIAALVRQVVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 15

TGTCGCCTGGCCCTCGCC**ATG**CAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA
CTGGGGGGCGCCACGGCCTCTTTCTGAGGAGCCGCGCCGCTTAGCGTGGCCCCAGGGACTACCTGAACCAC
TATCCCGTGTTTGTGGGCAGCGGGCCCGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCACG
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTCGGATGAAG
GGCAAACAGGAGGGCGAGTGTGAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC
GGTTCACACGCCTTCAACCCGGTGTGCGCCAACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC
GGTATGGCCCGCTGCCCGTACGACCCCAAGCACGCCAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT
ACTGTTACCGACTTCCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGCCACCCCTGCGCACCGTG
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCGAGTGTGCAAGAAC
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGTCTTCTGAAGGCGCGGCTCAACTGCTCTGTA
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCCGGCCCGTG
GTCCTGGCCGTTTTTTTCCACGCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCGAGTCCATCTGGACGCCGGTGGCGGAGGATCAG
GTGCCTCGACCCCGGCCCGGGTGTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC
ATCCTCAACTTTGTCAAGACCCACCCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG
CGGACCCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCTGGGGCAACCAGACCGTT
GTCTTCTGCGGTCTGAGGCGGGGACGGTCTCAAGTTCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT
GGGCTCAGTGTCTTCTGGAGGAGTTTGAAGCTTACCGGCCGGACAGGTGTGGACGGCCCGGCGGTGGCGAGACA
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCCGCTGCGTGGTC
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC
GGGTGGGCCCCCGACGGCTCCTGCATCTTCTCAGCCCGGGCACCAGAGCCGCTTTGAGCAGGACGTGTCCGGG
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG
TCGGTGAACCTGCTGGTAACGTCTCGTGGTGGCGGCTTCTGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC
TGGTTCTGCGGCTCCGTGAGCGGCGGGAGCTGGCCCGGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG
GGCGAGGCGGTGCTGAGCGTCAGCCGCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGGCGGAGGCGGT
GGCGGTGGCGCCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG
CTGACGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCCGAGCAGACGCCGCTGCCGAGAAGCGC
CTGCCACTCCGCACCCGCACCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCTGCTCCCGGCC
TCCGCTTCATCCTCCCTCCTGCTGCTGGCGCCCGCCGGGCCCGAGCAGCCCCCGCGCCTGGGGAGCCGACC
CCCGACGGCCGCTCTATGCTGCCCGGCCCGGCCGCGCCTCCACGGCGACTTCCCGCTCACCCCCACGCCAGC
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCTTGGACCCAGCCTCAGCCGCCGATGGCTCCCGCGG
CCCTGGAGCCCCCGCCCGACGGGCGAGCCTGAGGAGGCCACTGGGCCCCACGCCCTCCGGCCGCCACCCCTGCGC
CGCACCCACACGTTCAACAGCGGCGAGGCCCGGCCCTGGGGACCGCCACCGCGGCTGCCACGCCCGGCCGGGACA
GACTTGGCCACCTCCTCCCCATGCGGGGGGCGGACAGGACTGCGCCCCCGTGCCCT**TAG**GCCGGGGGGCCCCCG
ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAACGCCGGGGGCCGGGGCAACTCCG
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAACCAG
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGTTTTGGGGTGGGTGGGCGGGAGGACTTTGCTATG
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGCAGTTTTGGTTTTCTTTTTCGGTTTTCTAACC
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGCAGGGGAGGCTTGGACGCCGTGGGGAATGGGGGGCCACAG
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG
TGCCTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGGTCTCCGAGGTGCCGTTAGGAGTTTGAAC
CCCCCCCCACTCTGCAGAGGGAAGCGGGGACAATGCCGGGGTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA
ATACGGCCCCAGGGTGGTGAGAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCTCCCCAGCCCCCTCCCCATCAAT
AAAACCTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLGGAGHLFPEEPPLSVAPRDYLNHYPVFVGSGPGRLTPAEGA
DDLNIQVRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG
ECRNFVKVLLLRDESTLFVCGSNAFNVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGSFVYFFREI
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCVPGDSHFYFNVLQAVTG
VVSLGGRPVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPVEDQVPR
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHPWILRTLMRHQLTRVAVDV
GAGPWGNQTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ
RLLSLELDAASGGLLAAPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGCIFLSPG
TRAAFEQDVSGASTSGLGDCGTGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGRGGGGGGGAGVPPEALLA
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLP
SASSLLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFLTPHASPDRRRVVSAPTG
PLDPASAADGLPRPWSPPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG
TDLAHLPPYGGADRTAPPVP

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCTCGGCCGGGACAGC
AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGGCACGGGCTTTGATTGTCCTGGGGTTCG
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC
ATTTATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCCTAGAGTTGGAGTCCAGGTTTTAGAC
CGAAAAGATGGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT
GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCATATATTTTAAAAGGGCCGGTTT
ACCATGAGAACTGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCCTACACCTTAA
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAAATTTTCATGGAT
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG
GAAACCATGGGCCGGGTAAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG
GGAAAGCAAAAATTCCTACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTACCAACTTTTTCTTC
TTTAAACACGATGAAAACCTGTATGGTCCCATTGTGAAACATATTTTCATTTTTTGATTTCTT
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACT
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC
TGAGGACGACCTCTTCCCTTGTAAGTGGCATAGGAAAAAGACCAAAGATGAACTCTGATATG
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAACTAAAAAGAAGAATT
TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA
TAAAACCACCTTTATTTTAAAGGAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLARYFYIQAVDTSGNKF
TSSPGEKVFQVKVSAPEEQFTRVGVQVLDRKDGSFIVRYRMYASYKNLKVVEIKFQGQHVAKS
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNLSDLLEKLKWAKDHDEEAKK
IAKAGQEFARNNLMGDDIFCYFFKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK
KTKDEL

Important features of the protein:

Signal peptide:

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA
GCCTAGCGTGTCCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTCGTTCTCTGCC
AGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCTAACTG
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG
ATGATTTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA
AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGCGACGTCATCAGGAACCTCAATTCTC
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT
TATGGAGATGAAACCTGGGTAAATTATTCCTCAAAGCATTTTGTGGAATATGATGGAACAAC
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC
CACATTTTCAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA
TCCAAAGCACGTCCA**ATAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG
CAGTTGAGATTTTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAAATGTCAGAAAGATTGCATGGGAACT
GGATCAGACTGTACTTGGAGGAAAAGCATTCAAGAGTCCTATTCAACCTGGGCTCCAAGGTT
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCA
GTTCTCACCCCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGT
CCCCTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG
TGTCCCGACACAGGTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACACAGAGGAACAAGCCC
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA
CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTTCGTTAGCTGGGGAGTG
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATC
CCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGCACCTCGGGC
CCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPP
PLFSKVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFFVS
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNSPLIGQKLSEMDSVLMKIHT
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 21

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATG
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC
AAATGCAACGCCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA
TCGGCAGGTCCCGACGAGTCCAGTGTACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG
CACCACCGAGGGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT
CCCCGAGCACTACAGGTCCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC
ATAGACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCCTTGCTGCTTCAGC
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSL
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR
PSCTTEGTTSPWTAIDLQGSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVLGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG
GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCTATGGCTGT
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT
CCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAG
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATAACCGGAATTTGCTCA
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTT
CAAATTTTAATGGATGATCCCTTTTCTAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA
TGATCACGCGCCAGTATTTTCTAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT
GATATATCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT
TAACCCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCAGGCTCTGTATGAGACCCAGGC
TCCAGAAAACAGCCCCATTGGGTTCTTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG
GAGTCAACGCGGAAGTATCCTATTCATTTTTTGATGCCTCAGAAAATATTCGAACGACCTTT
CAAATCAATCCTTTTTTCTGGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGGTTT
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTTCCAAC
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC
TGGAGAAAATGGAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT
CTGTGGAGAATTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACAT
AACGGTCTTGGTCTCCGACGTCAATGACAACGCCCCCGCTTACCCCAAACCTCCTACACCC
TGTTTCGTCCGCGAGAACAACAGCCCCGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGA
GACTCGGGCACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAAGACCCGCACCTGCC
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCGCTGG
ACTACGAGGCCCTGCAGGCTTTTCGAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCG
CTGAGCAGAGAGGCGCTGGTGCGCGTGCTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGT
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTTCGGTGTGTGGGCGCACAATGGGGA
GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAGCCAAGCACAGGCTCGTGGTGCTTG
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC
GGCTTCTCCCAGCCCTACCTGCCTCTCCCGGAGGCGGGCCCCGGCCAGGCCCAGGCCGAGGC
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCCTCCTCT
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG
TGCTCGGTGCCCCGAGGGTCTTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT
GTCCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTTCAAGT
TCTTGAAACCAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT
TCCACCTTCCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTTTAGTTTCATATAC
TTTTGGTGTGTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT
TTTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTTCTAAATGATAGTGTT
AAGGTTTTTAATCTTTCCAACCTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT
CTGAGGTTTTGATTCATTTTCTAGAGCTTGCACTCTCATGATTCTAATCACTTCTGTCTATAGTG
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTTCTATATATT
CGTGTTTGAAAACCATGTCAATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC
CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGGCCAATATTTT
CTTATGTTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAATAAAAAAAAAAAAAA

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLEFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGD
EGMIYPELVLDKALDREEQGELSLTLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYE
TQAPENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND
RDSGENGKMVCYIQENLPFLKPSVENFYILITEGALDREIRAENITITVTDLGTPLRKTE
HNITVLVSDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDP
HLPLASLV SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAH
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVLDGFSQPYLPLPEAAPAQAO
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGLVDVRGA
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

[illegible][illegible]

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESD
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELGSDPTK
GTVCFYGHLDVQPADRGDGLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD
LPVNIKFIIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY
FMVEVKCRDQDFHSGTFFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKS VVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF
AAFFLEMAQLH

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

273-292

N-glycosylation sites.

amino acids 322-326, 382-386, 402-406

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 400-404

N-myristoylation sites.

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,
351-357

Cell attachment sequence.

amino acids 140-143

ArgE / dapE / ACY1 / CPG:

amino acids 156-167

FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**ATG**GGACCTGTGCGGTT
GGGAATATTGCTTTTTCCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG
AGGACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG
CTACAGGCGGAACTGAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC
TTCCACCATCAGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAG
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA
GCAAACCGTGAAGGAGAATGGGACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGG
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT
GCTCAACTTTCTATATCGCTATTAACTTTTTTTCTTTTTTTCTA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL
ELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK
GLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEG
HVLPAEAETACLQETWTGKEITDGEKTEGEEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 29

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG
GGAACATTGGCTGCAAGGTTGTTCTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTAC
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAATGG
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA
AACCAGGCAGAGA**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC
TGCTCACCACCGACGATGTGGGTATGGAACCCCTCTGGATACAGAACCCCTTCTTTTCCAA
ATTAAAAAAAATCATCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK
KGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSWKMDRFLNRFHL
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 169-173

Tyrosine kinase phosphorylation site.

amino acids 59-68

N-myristoylation sites.

amino acids 54-60, 83-89, 130-136

Phosphatidylethanolamine signature.

amino acids 113-157

FIGURE 31

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTTCAGTCCCCTGGACTGTAGATAAAGA
CCCTTTCTTGCCAGGTGCTGAGACAACCACACT**ATG**AGAGGGCACTCCAGGAGACGCTGATGG
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG
TATTGTGAGAAGGTTGGAGAACAGCCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA
CTGAACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT
TTTCGTCTACATTTTCTTAGTGTCATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCCTCTCAAGCTGGTGCTGTGTAG
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT
ATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAGACCTTGTAACA
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA
TCCAGTCTTTATATGTTGCCAATATACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAG
ACCTTGTAACAATAAATAATTCTTGTGTAAAGTTAAATCATTTTTGTCCTAATTGTAATGTG
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACCTGATATAAA
ATAAAGAAAGAGTAAACTG

FIGURE 32

MRGTPGDADGGGRAVYQSITVAVITCKYPEALEQGRGDPIYLGIONPEMCLYCEKVGEQPTL
QLKEQKIMDLYGQPEPVKPFIFYRAKTGRTSTLESVAFPDWFIASSKRDQPIILTSELGKSY
NTAFELNIND

Signal sequence:

amino acids 1-17

N-myristoylation site.

amino acids 10-16

Cell attachment sequence.

amino acids 36-39

FIGURE 33

GCGAGGCTGCACCAGCGCCTGGCACC**ATG**AGGACGCCTGGGCCTCTGCCCCGTGCTGCTGCTG
CTCCTGGCGGGAGCCCCCGCCGCGCGGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC
TAAGGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCTACCCAGGAACCTCCTTTGAGCATAGA
GTTAGCAACCATGCTTCTCATTCCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA
TTTTGAGAACATGCACAATAGTATGTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC
AGACTTTCTTCACTGTCTTTTCAATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC
ACATGGA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA93011

><subunit 1 of 1, 136 aa, 1 stop

><MW: 15577, pI: 8.88, NX(S/T): 0

MRTPGPLPVLLLLLAGAPAAPPTPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLDDCNALEY
IPVTTVLPRQR

Important features of the protein:

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

FIGURE 35

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCA
GCCGCCCAGTCCCGGCCCCCTCTCCCGCCCCACACCCACCCTCCTGGCTCTTCCTGTTTTTAC
TCCTCCTTTTTCATTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA
AGCCGAGCGTGGAAGAATGGGGGTTCCCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGC
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG
AAAAGTATTGATTCAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT
CCTACCTTGAAAACCTTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAAT
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAA
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAAACACTTC
TAATTCTGTGATTAAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT
TAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 36

MGFLGTGTWILVLVLPIQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIKEKVTMAAIQDGLAKGENDET
VSNTLTLTNGLERRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFV
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLFPPAPSEKSHEETDSTKEE
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS
KMRDFINKQADAYVEKGILDKEEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

[illegible][illegible]

FIGURE 38

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR
LAWYLDGQLQEASTSRLLSVGGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTSASLPAPGPSRHPSLISSDSNNLKLNNVRLP
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY
RVSSVSSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 39

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGCG**ATG**TGGAGCGC
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA
GCAATCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGGCG
GCTCGGAGGGCGGGTGCCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA
GGAGGTGAGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGA**GTGTGTGGATGGATGGGTGGATGGAGG
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL
SNNQEVSAFGEDGEGDDLDLWTVRCGQHWEREAARFQHVGTSVFLSVTGEQYGSPIRGQH
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 41

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACCACAG
ACGTGAGCCACTCCACCCAGCCTAAAACTTCATCTTCTTTGGATGAGATGAACACTTTTAAC
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACTCTAAGGAGGAGCACTGACT
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT
CGTCATCATGTCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC
ACGAGCCAAGTACCTCAAGAGACATGGCTTCTAACATCTCAGATGAAACCCAAGACCATGAT
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAACCTGGGAAT
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAATAAAAAAAAAAAAAA

FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867
><subunit 1 of 1, 194 aa, 1 stop
><MW: 21431, pI: 8.57, NX(S/T): 0
MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM
PYLLKYQPMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA
KYLKRHGF

Important features of the protein:

Signal peptide:

amino acids 1-19

N-myristoylation sites.

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

Amidation site.

amino acids 40-44

FIGURE 43

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**AAAG
CCCTTATGCTGCTCACCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**
ACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT
CTGTATCCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG
TTCCGAGTGGTCTCCTCATCCATCCTTCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT
CCCTTCCCCTTCCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA
AACCAGGCTCCCATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAAA

FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN

LRCGTPEEPCQEAFNQTNRKLGGLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 45

ACGGGCCGCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCA
GTCGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT
ACCGCACCCAGGTTTCGGC[.]CCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**AT**
GGCCGCGAGCCTGCGGGCCGGGAGCGGGCCGGGTACTGCTTGCTCCTCGGCTTGCATTTGTTTC
TGCTGACCGCGGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCTCCACTATGACCGCTATAACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAAGTCTATAAGCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA
TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAGGAGACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTTCATCACTTTCTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAG
GGGATATTCAAAGTTCTGTGGTGTATGTCCAGTGTAGCTTTTTTGTATTCTATTATTTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA
TATTGCAGTTTTTGAAGTGATCATTACTGTGGAATGCTAAAATAACATTAATTTCTAAAC
CTGTGATGCCCTAAGAAGCATTAAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTTCAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

FIGURE 46

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP
QLKCVGGTAGCDSYTPKVIQCQNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY
VLRGSCGLEYNLDYTELGLQKLKESGKQHGFAFSFYKSSADSCNMSGGLITIVVLLGIA
FVVYKLFSLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPL
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318